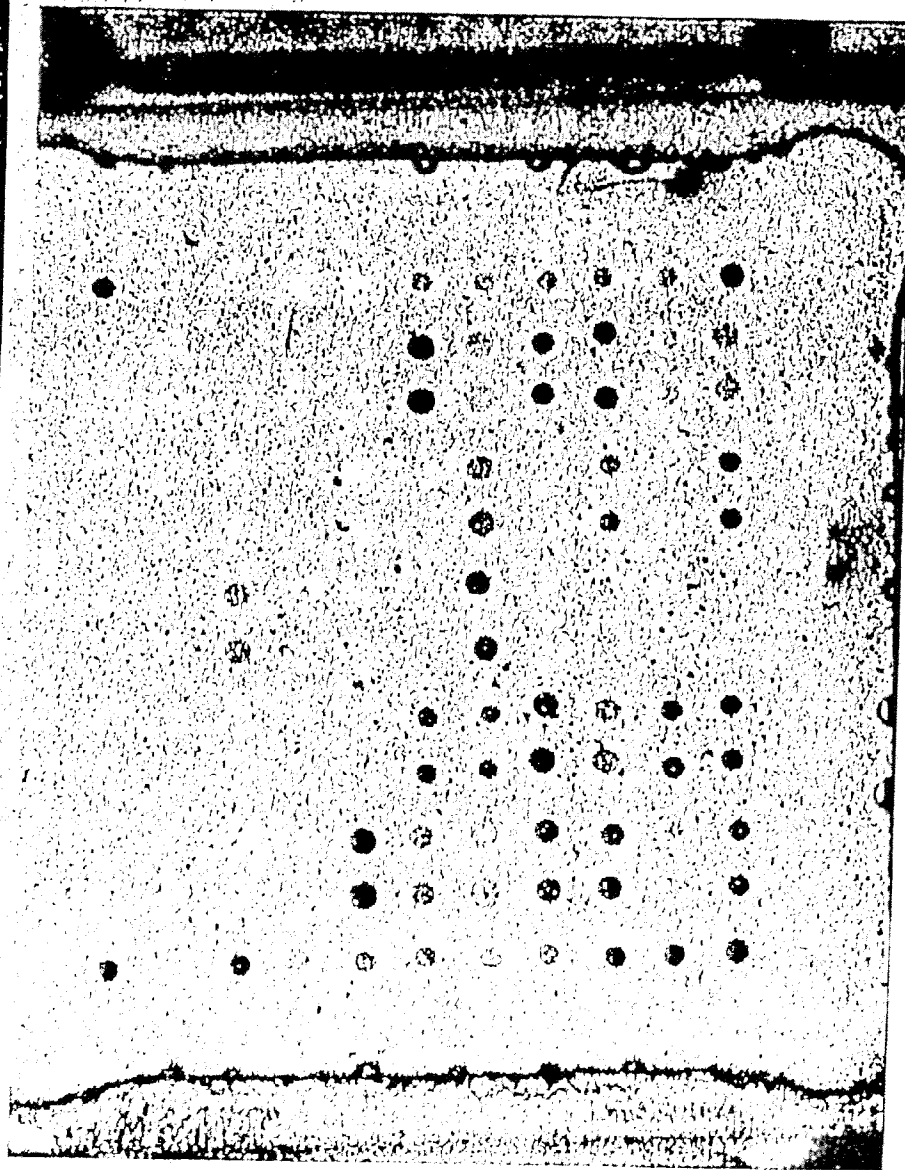FIGURE 1
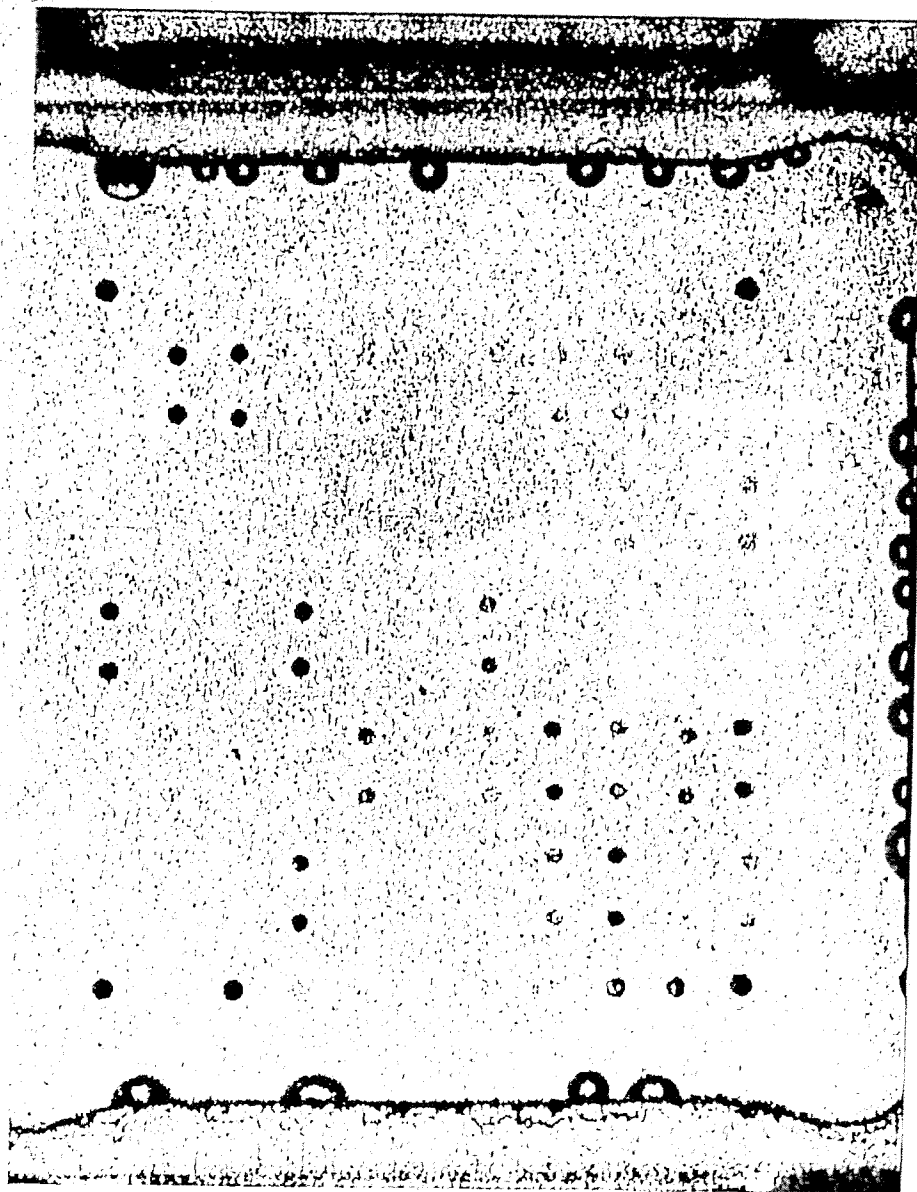

P. aeruginosa AT-Chip

ZW117

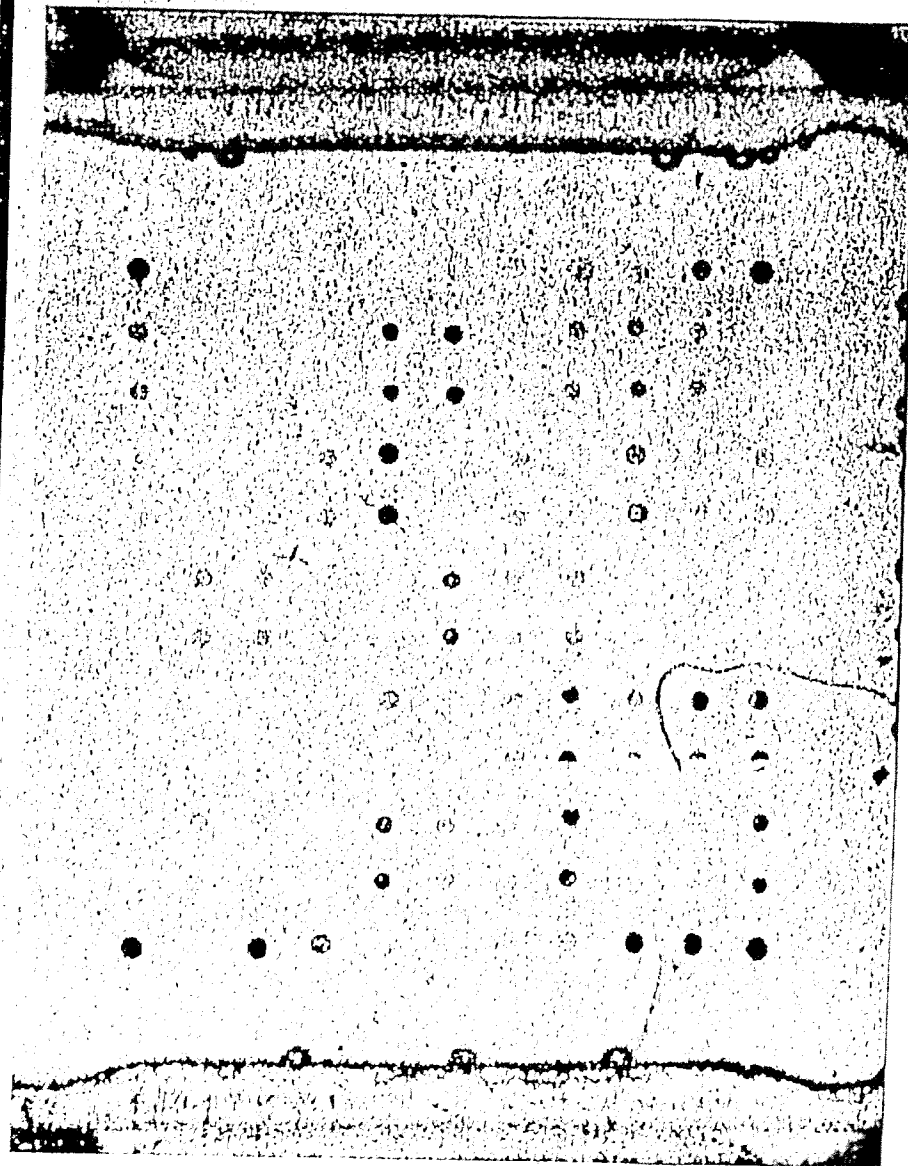FIGURE 2

P. aeruginosa AT-Chip

RP17

FIGURE 3
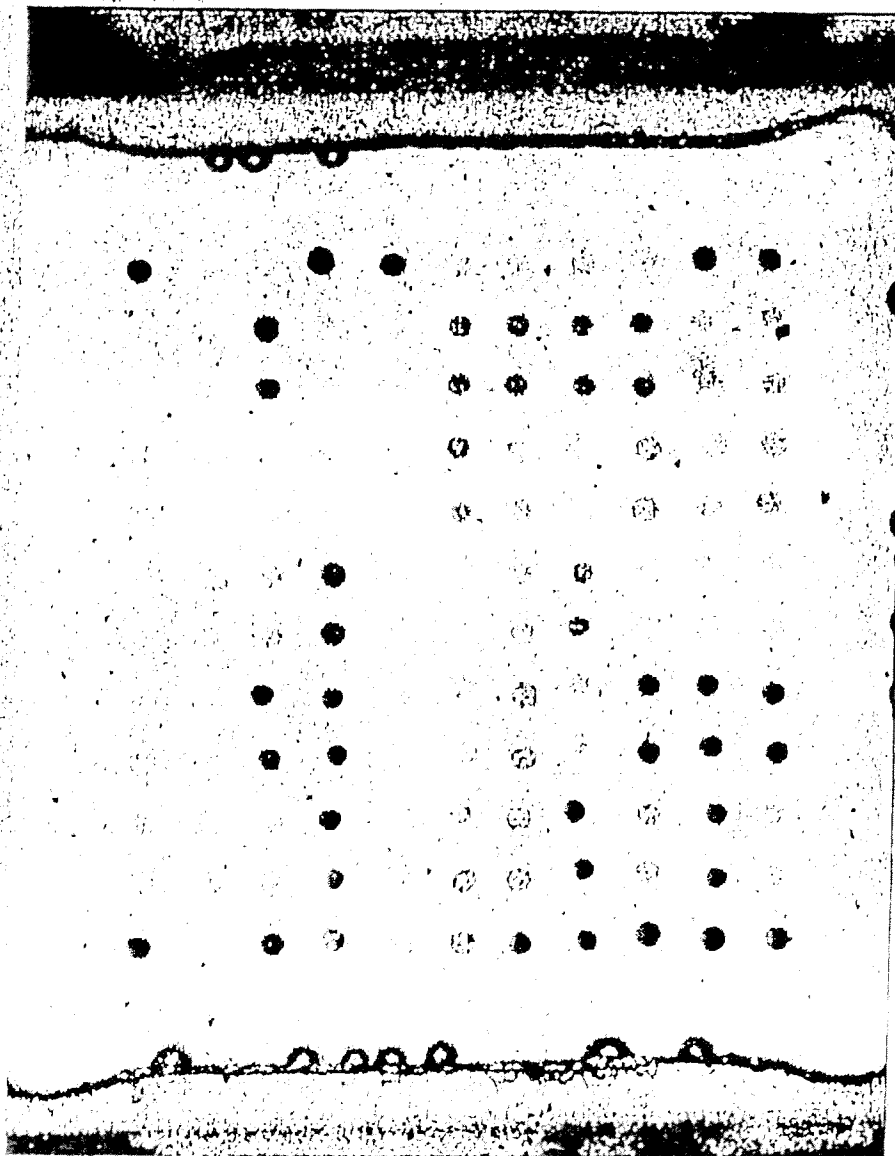
FIGURE 4

P. aeruginosa AT-Chip

SG17M
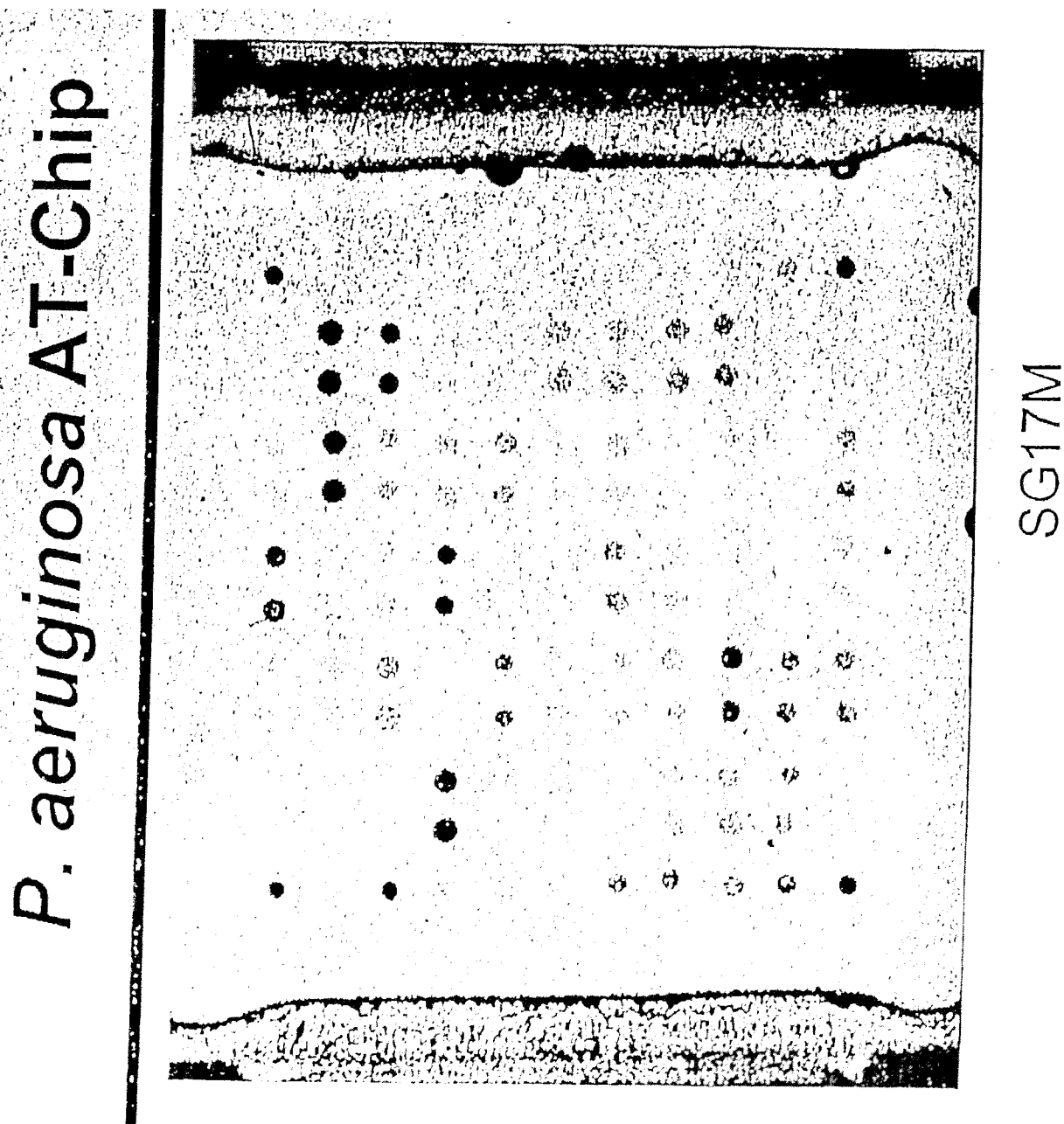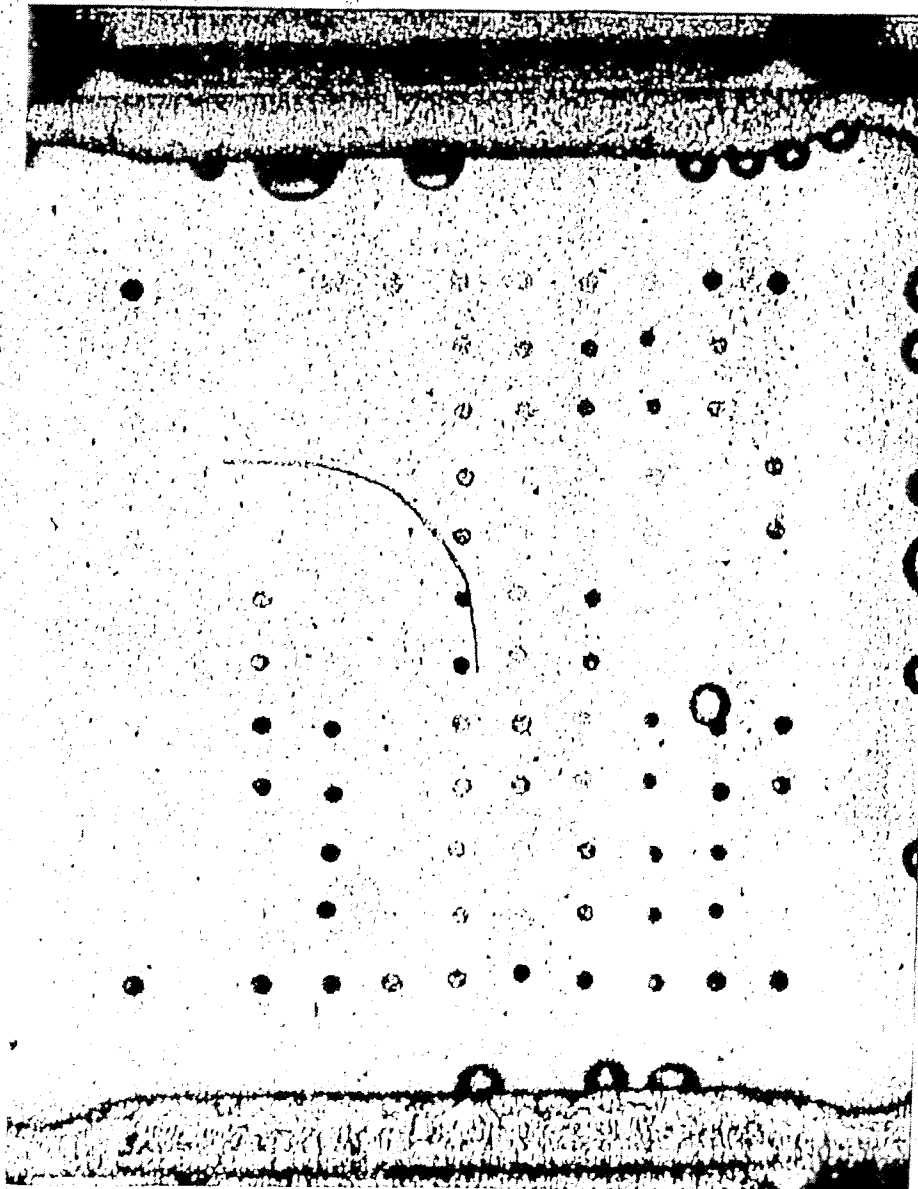
FIGURE 5

FIGURE 6

FIGURE 7
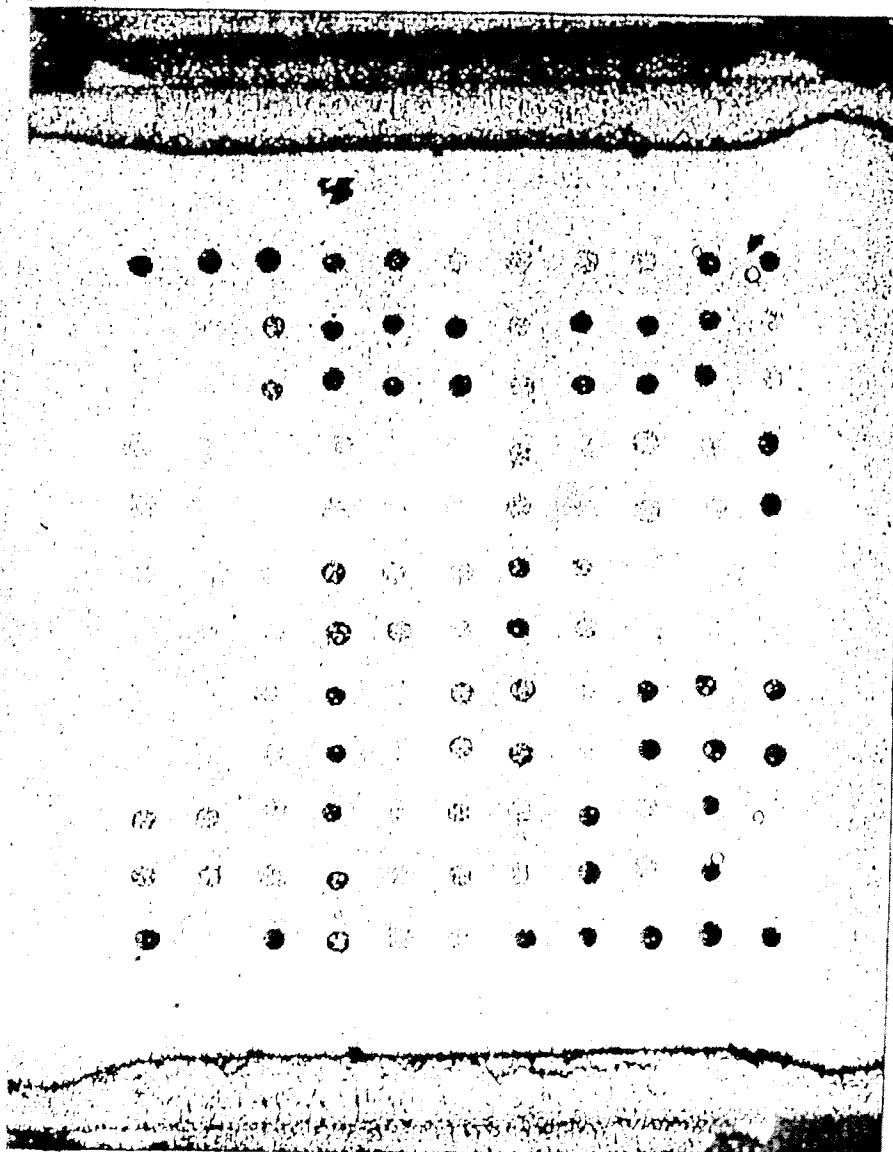
P. aeruginosa AT-Chip

PT12

FIGURE 8
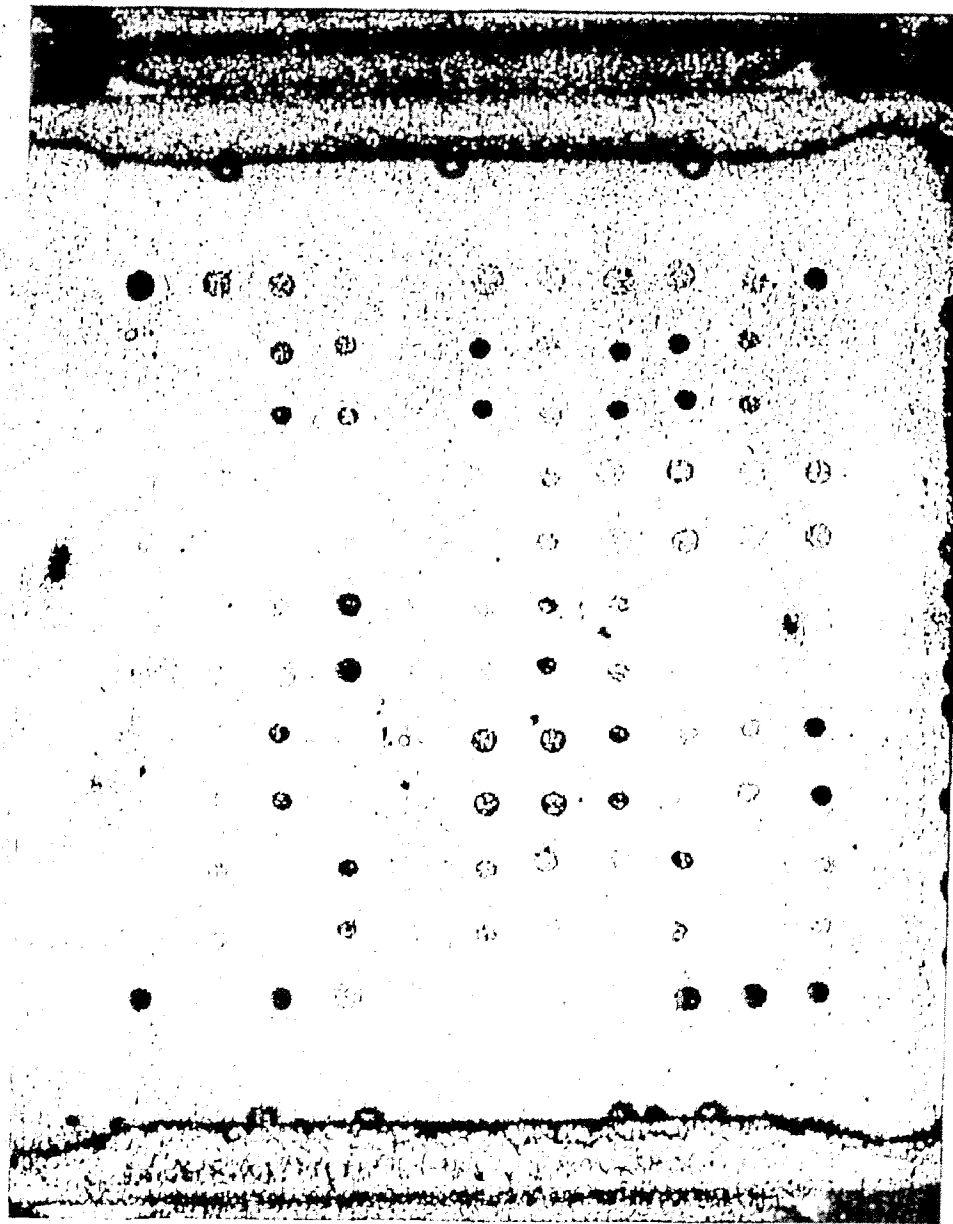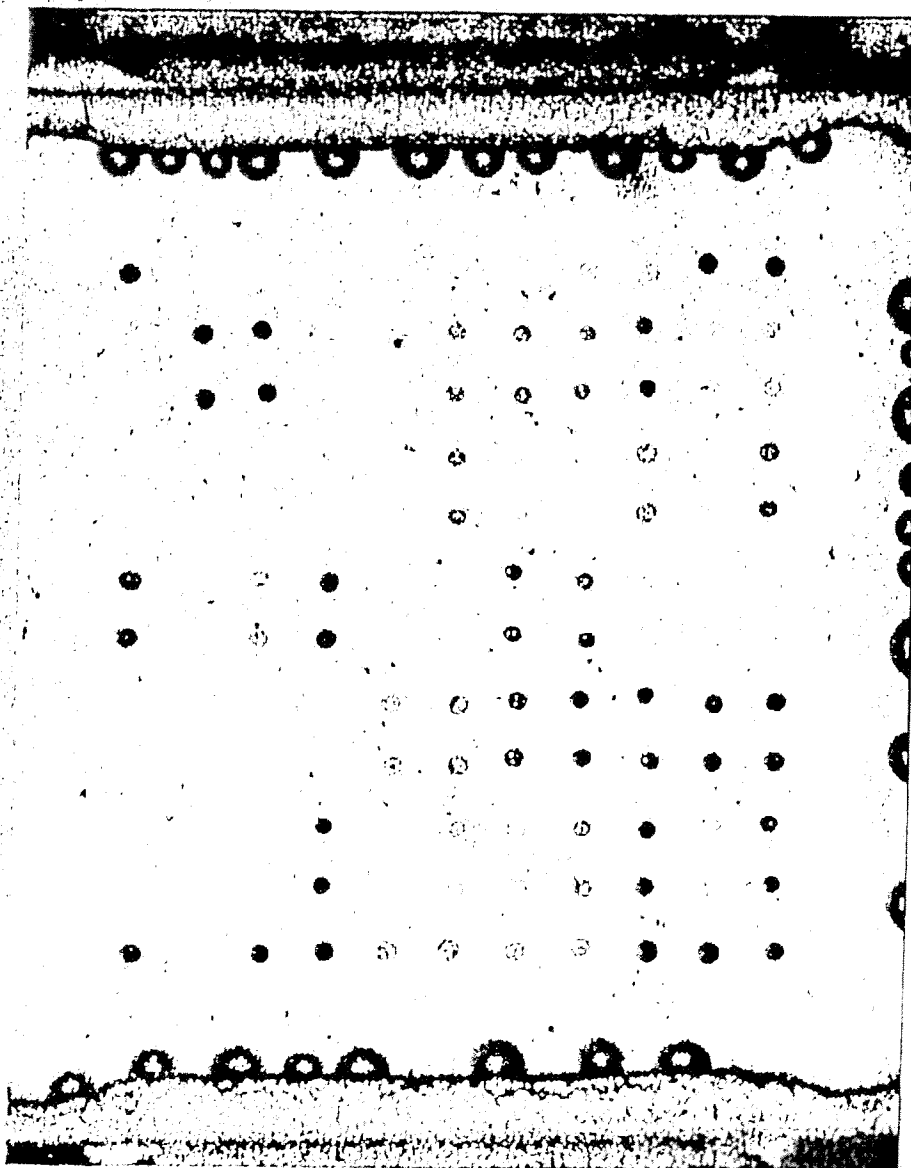
FIGURE 9

FIGURE 10

P. aeruginosa AT-Chip
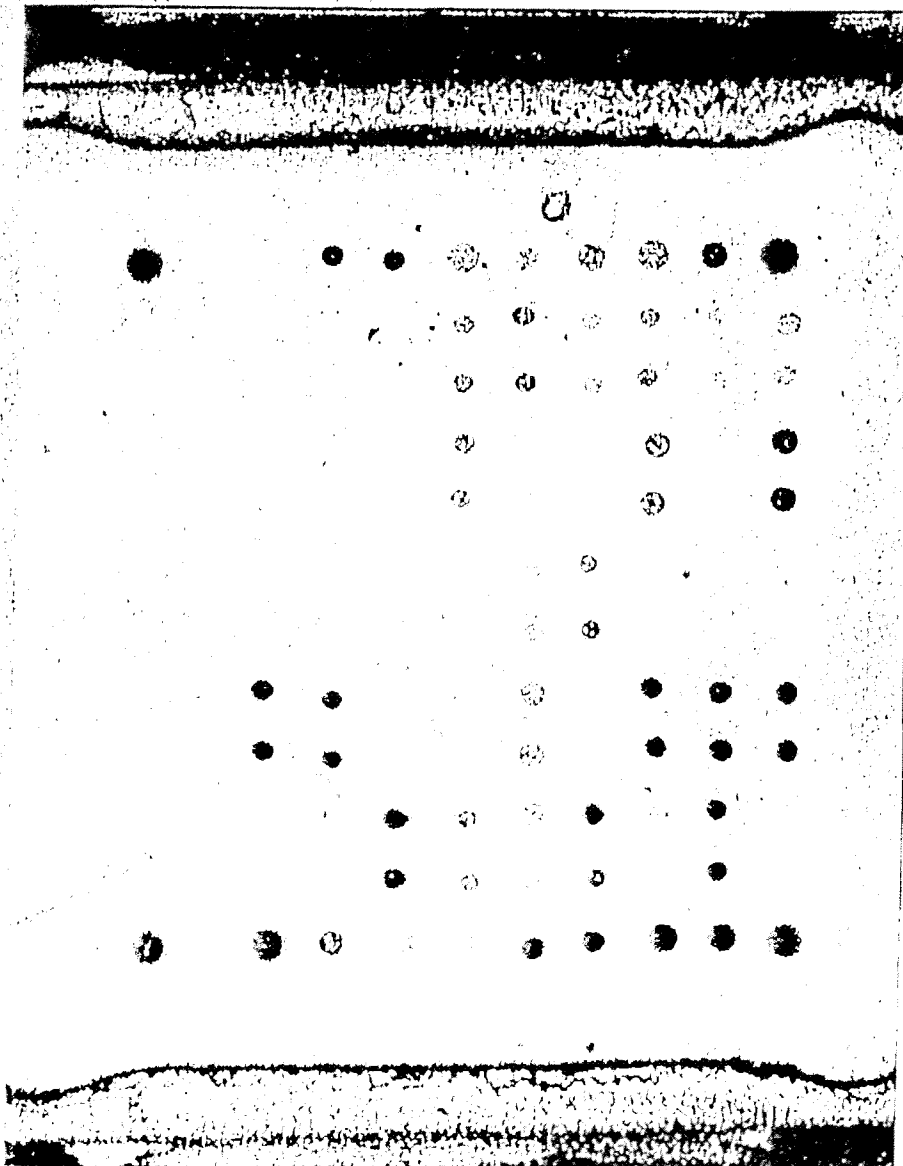
ZW85

FIGURE 11
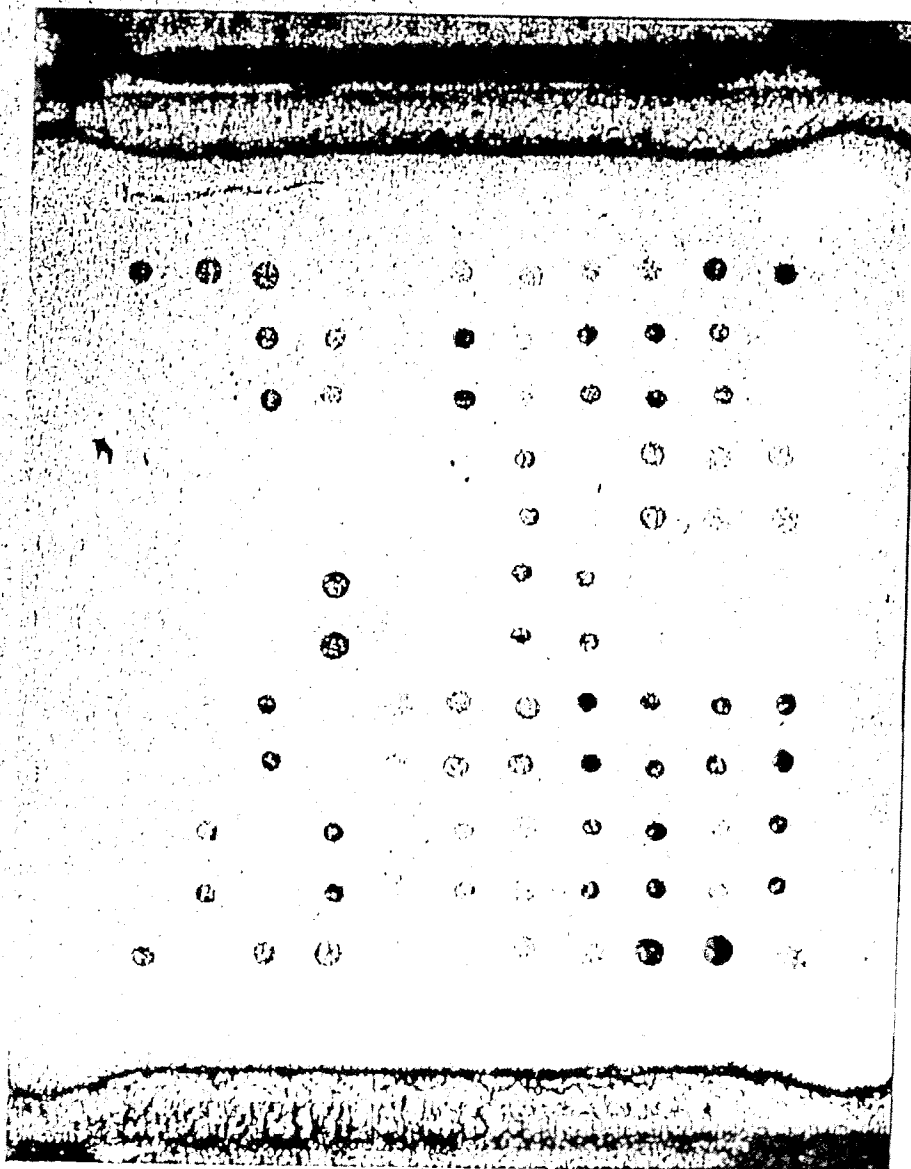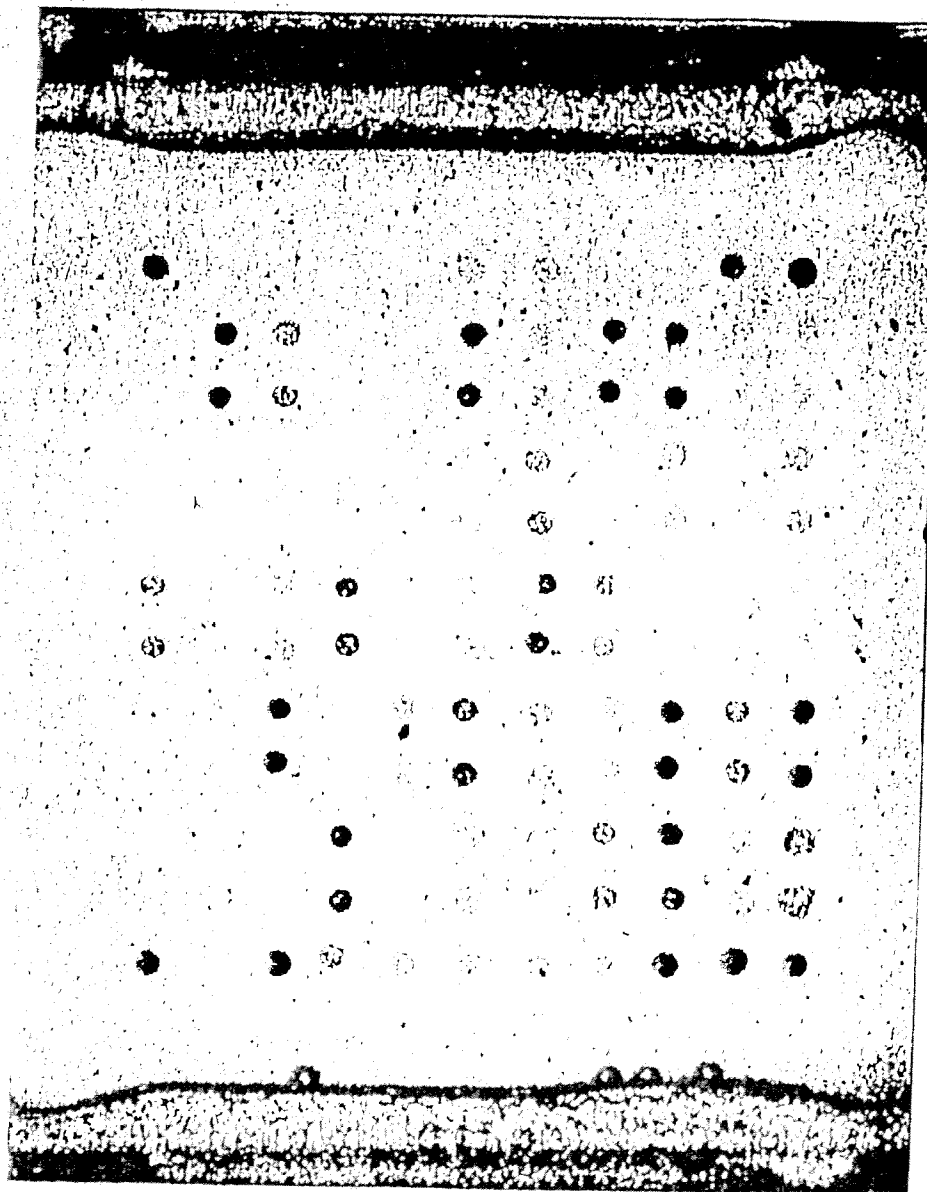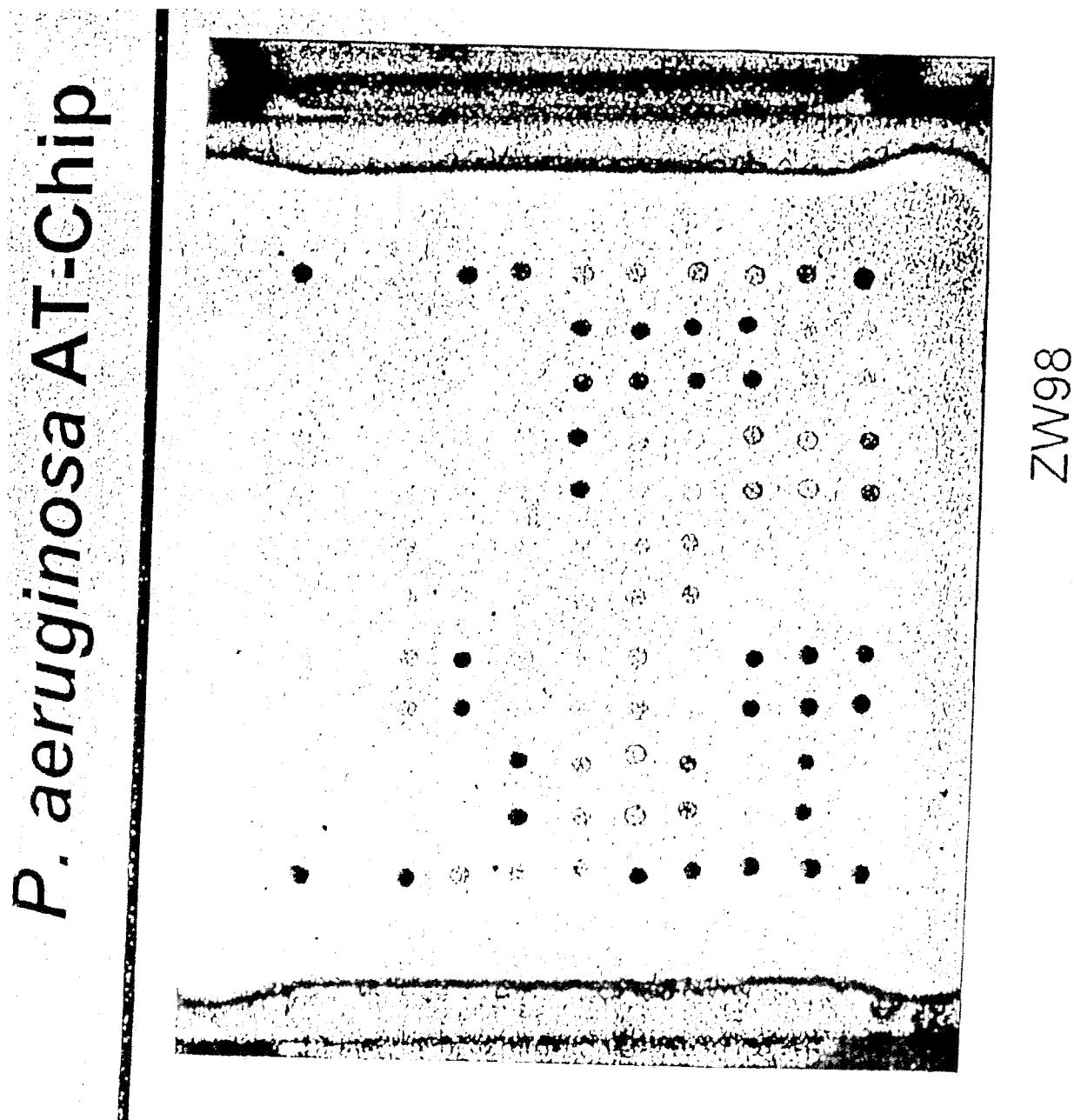
FIGURE 12
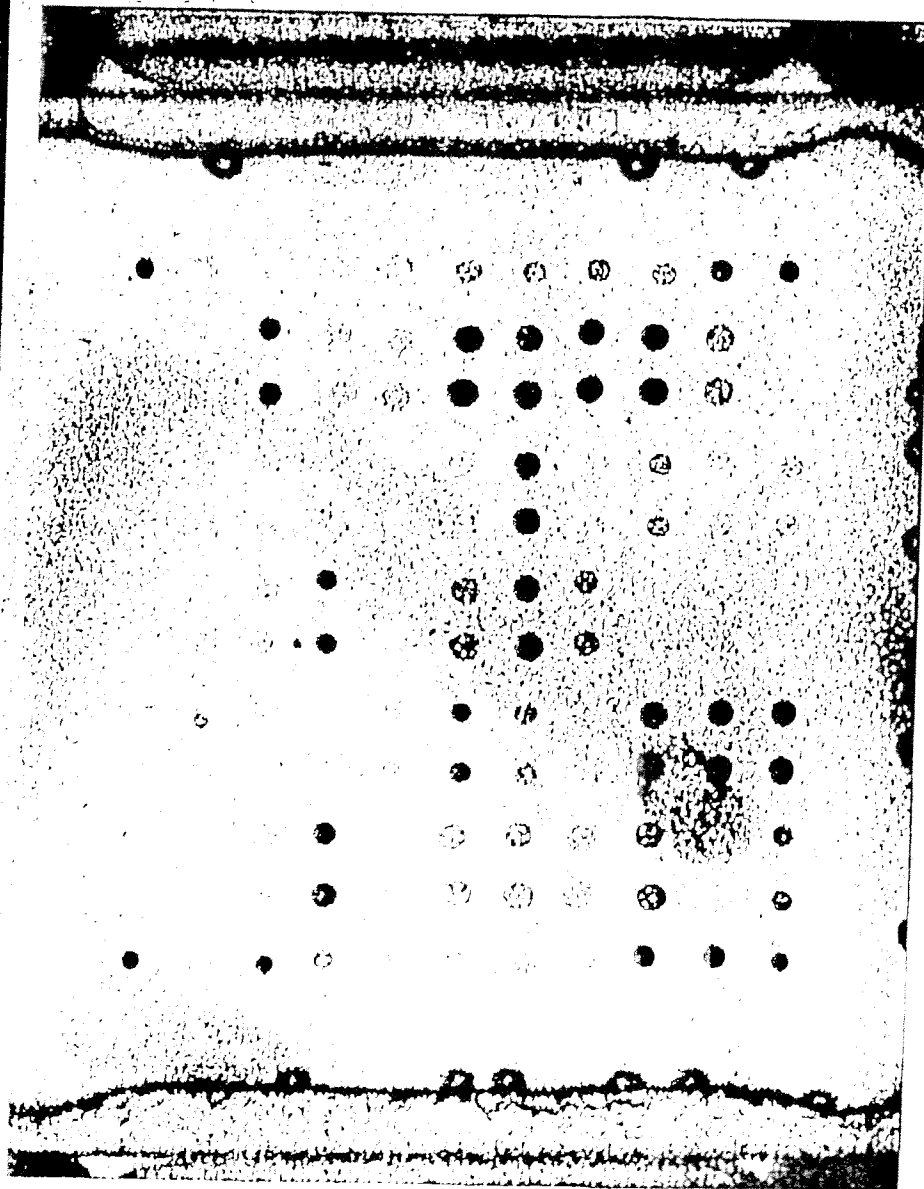
FIGURE 13

FIGURE 14

FIGURE 15

P. aeruginosa AT-Chip
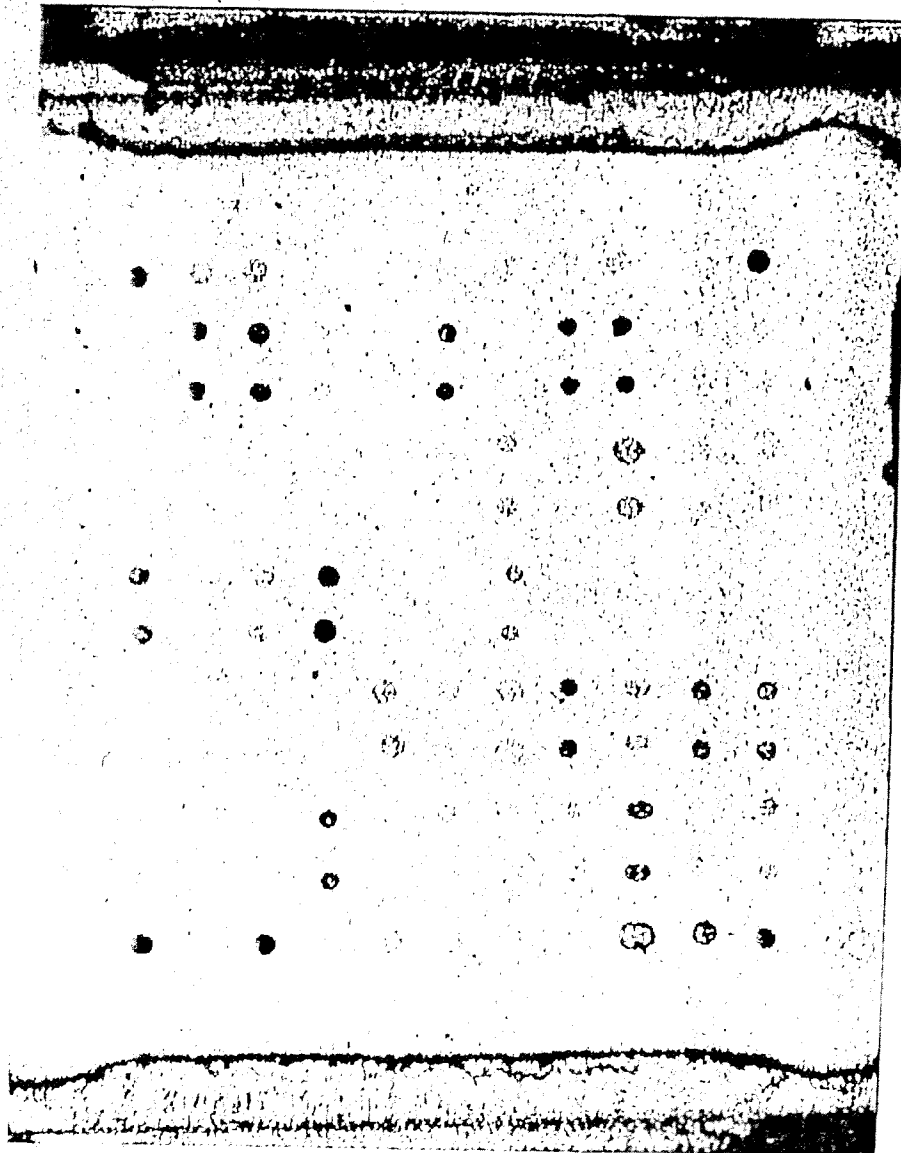
ATCC15522

FIGURE 16
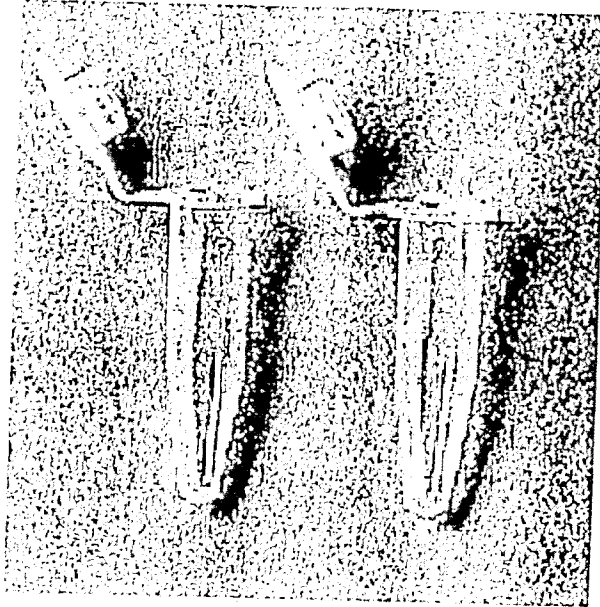
FIGURE 17A

47-1/23
ACGCGGATGTCCTGGATTTGG

47-1/39
CTGAAGAAGGGGCGCTACGCG

47-2/22
GCGTACCGGGCAAGGTGATAG

47-2/52
CTCGGTGAAACATCGGGAGGG

C45/18
TCATCCAGCAAGCCATTGCGC

C45/60a
GGAGTCGCTTTCCGCCATCG

C45/60b
TGGAGTCGCTTTCCGCCATCG

C46/15
AAGGGCGTTTCACGCTGACGC

C46/22
ATCCGGAAGGGCGTTTCACG

C46/88
TCCACACCTCAGACTTCGGCG

C47-1/43
TATTGACGACCTACCGCGCGC

C47-2/56a
GCAACTGATGTTCGCCCAGC

C47-2/56b
CGCAACTGATGTTCGCCCAGC

C47-2/59
ACACGCAACTGATGTTCGCCC

CIS-4/36
TGTCCCGGCTCAGTTCAACG

CIS-4/50
AACACCTTGGCGTTTGTCCC

CIS-4/51
GCAACACCTTGGCGTTTGTCC

CIS-5/4
TCAAGCTCGTTGTGGACCGC

CIS-5/48
GTTACGACGGCGTGCTGTCGG

CSP-1/39a
ACGCAACGTATTCGGCGACCC

CSP-1/39b
CGCAACGTATTCGGCGACCC

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FIGURE 17B

fliAT/28
AGCTGATGGTATCGCCGTCGC

fliAT/72
CTAGTGATCGCACCGGAGCC

oriC/20
AGCCTCGACACCGGTTCTCG

oriC/54
TCGTTCATCCCCAGGCTTCG

oriC/59
ACCATCTCGTTCATCCCCAGG

oprL/53
TTCTGAGCCCAGGACTGCTCG

oprL/65
TCGACGCGACGGTTCTGAGCC

fliCb/36
TGACGTTCTCGCCGGTAGCG

fliCb/65
CAGTAGCGGTACCGGTCTGCG

fliCb/66
CAGTAGCGGTACCGGTCTGC

alkAG/27
TTCCTCGCCGGCATAGTAGGC

alkGA/32

alkGA/51
CGAGGACGAGGCATCTTCCGG

citAG/4
GCAGGTAGCAGGTTTCCAGG

citAG/46
AACTGTTCCTTCTGCGCGGCG

citGC/8
TGATCGGCTTGGTCTCGCAGG

citGC/11
GCTGATCGGCTTGGTCTCGC

citGC/75
GAGGCGTTCTGCTCGTGGTCG

oprI/12
TTTTTCCAGCATGCGCAGGG

oprI/17
GCTGGCTTTTTCCAGCATGCG

oprI/22
TTGCGGCTGGCTTTTTCCAGC

- 18 -

FIGURE 17C

```
am7CA/1
TTGGGATAGTTGCGGTTGGC

am7CA/27
CGTAGGCGATCTTCACCCGC

am7CA/29
TGGCGTAGGCGATCTTCACCC

am3CT/21
GGCGAGATAGCCGAACAGGC

am3CT/22
GCGGCGAGATAGCCGAACAGG

am3CT/69
CACTTGCTGCTCCATGAGCC

am2CT/35
GAGGTCGAGCAGGCTGATGC

am2CT/42
TAGGTCGCGAGGTCGAGCAGG

am2CT/92
GTCCTTCTGCACCGAGTCGG

am1GA/49
CGCATCTTGTCCTGGGTCAGG

am1GA/58
TCGTCGAGGCGCATCTTGTCC

am45/1
ACGTCGAGGTGGGTCTGTTCG

am45/96
GTAGCCTTCGGCATCCAGCG

am6TC/60
TCGGCATTGGGATAGTTGCGG

GI11/15
CCTCCTGTCTCATGCCGATGC

GI11/59
GCATTCGCCACGGAAGGAAGG

GI11/71
GAAGGCATCATGGCATTCGCC

GI18/62
GTCATGGGGTTTCCCAGAGACC

fliCa/41
GATCGCGATGTCGACGGTGCC

fliCa/42
CGATCGCGATGTCGACGGTGC

fliCa/46
TGCCGATCGCGATGTCGACG
```

FIGURE 17D

SG-1/40
GACGAATACCCAGCTGCGTGG

SG-1/43
GCAGACGAATACCCAGCTGCG

SG-4/1
CGCGACGTCGTGACGTCAGC

SG-4/67
ACTTTCGGCTCTTCGGGCTGG

TB46/21
AGGTAGAGACTCGGGGGAACC

TB46/45
TCGTTTTCGGTCATGGCCAGG

TB471/22
TTCCGCGACGAACATCCGTGG

TB471/25
CGCTTCCGCGACGAACATCCG

TB472/36
GGATCGCTTCCGATAGGGCAGC

TB472/84
AGAGGCATGGGTCTGTACCG

TB473/34
TCTGTCAATCCCCTTTGGGG

TB473/41
AGCCCCTTTCTGTCAATCCCC

TB474/36
GGCTTCCTACCGAAGGTCAGG

TB474/41
TGAGGGCTTCCTACCGAAGG

exoS/31
TTCAAGGTCATGGGCAATGCC

exoS/37
AGTCCCTTCAAGGTCATGGGC

exoU/22
GCCGACTGAGCTGTAGCTCGG

exoU/23
GGCCGACTGAGCTGTAGCTCG

exoU/42
ACCAGACTGGTCAATGGTGG

flins/2
CCCGTGTTTCCGTAGACCTTGC

pKL11/49a
AGCAGTTACCCACAGCATGG

FIGURE 17E

pKL11/49b
CAGCAGTTACCCACAGCATGG

pKL3/47
CTACACTCCAACCGCTGGTCC

pKL3/50
GACCTACACTCCAACCGCTGG

pKL3/80
TTCCCTTGCTGCCGAGAAGC

pKL7/14
TAATAGGCGAGCCTGCCGTCC

47D7nw1a
TCCACGCCGAGGGACGTGCC

47D7nw1b
GCTCCACGCCGAGGGACGTGCC

C46-nw1a
CGCGGTGCTGGTTGCGCTGC

C46-nw1b
CCAATGCCCAGGGCCAGCGGA

C46-nw1c
CGCTGGCAGTTCCGCTGGCC

ExoSnw1a
CAGGGTCGCCAGCTCGCTCGCC

ExoSnw1b
AGGGTCGCCAGCTCGCTCGC

ExoUnw1a
AGTGATCTGCCGCGGCCCTGCC

ExoUnw1b
GTGATCTGCCGCGGCCCTGC

OrfA-1
GTTCCACAGGCGCTGCGGCGC

OrfA-2
GTTCCACAGGCGCTGCGGCG

OrfA-3
CAAAGCCCCTGGTCGCGCGG

OrfC-1
GCAGCTTTTCCACCGCCGGCGG

OrfI-1
AAACTGCCCCGCCCCCCATCC

OrfI-2
GGAAAAACTGCCCCGCCCCCC

OrfJ-1
ACGCTCGCAGCGCCTCACGCG

FIGURE 17F

```
OrfJ-2
GGCCTGGCTGCGAACGCTCGC
```

FIGURE 18A

Nr	tube	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spot-ID's
1	Pa-S_001	oriC_T-C_wt_1	GAAGCCCAGCAATTGCGTGTTTC	1	23	52,2	62,4	1,2,3
2	Pa-S_056	oriC_T-C_mut_1	GAAGCCCAGCAACTGCGTGTTTC	1	23	56,5	64,2	14,15
3	Pa-S_057	cpd_T-C_wt_1	GGTGCTGCAGGGTGTTCGGCCGG	1	23	69,6	69,6	4,5
4	Pa-S_058	cpd_T-C_mut_1	GGTGCTGCAGGGCGTTCGGCCGG	1	23	73,9	71,3	16,17
5	Pa-S_059	fliC_a_A-T_wt_1	CAAGATCGCGGCAGCGGGTCAAC	1	22	63,6	65,8	6,7
6	Pa-S_060	fliC_a_A-T_mut_1	CAAGATCGCGGCTGCGGGTCAAC	1	22	63,6	65,8	18,19
7	Pa-S_061	akB2_G-A_wt_1	TGCTGCAGGCGGGGGTGTGCTAT	1	23	65,2	67,8	8,9
8	Pa-S_062	akB2_G-A_mut_1	TGCTGCAGGCAGGGTGTGCTAT	1	23	60,9	66,0	20,21
9	Pa-S_063	akB2_A-G_wt_1	CCTCGGCCTGTTCCCACCGCTCTGG	1	25	72,0	72,8	10,11
10	Pa-S_064	akB2_A-G_mut_1	CTCGGCCTGTTCCGGCGCGCTCTGG	1	24	75,0	73,0	22,23
11	Pa-S_065	cltS_A-G_wt_1	TCGACGCACTGGCAGAGAATCCG	1	24	54,2	64,4	26,27
12	Pa-S_066	cltS_A-G_mut_1	GCGGCCACTGGGGGAGAAATCCG	1	23	60,9	66,0	38,39
13	Pa-S_067	cltS_G-C_wt_1	GCGGAAAACTTCCTGCACATGATGTT	1	26	46,2	63,2	28,29
14	Pa-S_068	cltS_G-C_mut_1	GCGGAAAACTTCCTCCACATGATGTT	1	26	46,2	63,2	40,41
15	Pa-S_069	cpd_T-C_wt_1	AGCTGCAGCAGACTGCTGACCGAGG	1	23	60,9	66,0	30,31
16	Pa-S_070	cpd_T-C_mut_1	AGCTGCAGCAGACCGCTGACCGAG	1	22	63,6	65,8	42,43
17	Pa-S_071	ampC_1_G-A_wt_1	ANGAGCACGGCGGCCGCCGGTCACGCC	1	25	76,0	74,5	32,33
18	Pa-S_072	ampC_1_G-A_mut_1	GAGAGGACGGCGGCCGCCAGGTGACGCCG	1	26	73,1	74,3	44,45
19	Pa-S_019	ampC_2_C-T_wt	GACAGGAATGCGGCCTCGACGACC	1	22	63,6	65,8	34,35
20	Pa-S_073	ampC_2_C-T_mut_1	CACGAGGATGCGTCGGACGACCG	1	23	60,9	66,0	46,47
21	Pa-S_021	ampC_3_C-T_wt	AAGCCCGCCCACGGCGCGGGCAG	1	22	77,3	71,4	50,51
22	Pa-S_073	ampC_3_C-T_mut_1	CAGCCGACCTATGGCGGGGCAG	1	23	73,9	71,3	62,63
23	Pa-S_075	ampC_4_G-A_wt_1	CCGTTCGAACGGGTCATGGAGCA	1	23	60,9	66,0	52,53
24	Pa-S_075	ampC_4_G-A_mut_1	GCCGTTCGAACGACTCATGGAGCA	1	24	58,3	66,1	64,65
25	Pa-S_077	ampC_5_G-C_wt_1	TGGAGCAGCAAGTGTTCCCCGGC	1	22	63,6	65,8	54,55

FIGURE 18B

Pa-S	Name	Sequence	Group	Length	Tm1	Tm2	SEQ IDs
Pa-S_070	ampC_5 G-C_mut_1	TGGAGGAGGAACTGTTCCCGGC	1	22	63,6	65,8	66,67
Pa-S_027	ampC_6 T-C_wt	GAACAAGACCGGTTCCACCAAGG	1	24	58,3	66,1	56,57
Pa-S_028	ampC_6 T-C_mut_1	AACAAGAAGGCCCCACCAAGG	1	23	60,9	66,0	58,69
Pa-S_029	ampC_7 C-A_wt	CGGACCTGGGCCTGGTGATCCT	1	22	68,2	67,7	58,59
Pa-S_030	A_mut_1	GCGAGCTGGGACGTGGTGATCCT	1	22	63,6	65,8	70,71
Pa-S_031	fliC b	GCCGACCACTGAACTCCAACTCG	2	24	58,3	66,1	74,75
Pa-S_032	fliC a	GTCGGTGACGGCCACCTACTTCA	2	23	56,5	64,2	66,87
Pa-S_033	exoS-1	CAGCCTGCGGTCAGTGTCCTCGG	3	22	68,2	67,7	76,77
Pa-S_034	exoU	CGCCAGTTGAGAACGGAGTCACC	3	24	58,3	66,1	88,89
Pa-S_035	C-47-1	GCGCGATCTTCTCCACTTCATCGG	3	24	54,2	64,4	78,79
Pa-S_036	C-47-2	GCCTCCGGCGATTGAACATGGTGAT	4	24	58,3	66,1	90,91
Pa-S_040	47D7-1	GTAGCCGGAGTCGAGCGGAATCATT	5	24	54,2	64,4	80,81
Pa-S_041	47D7-2	GTGAGCATGGAATGGCAGTCGTT	5	24	58,3	66,1	92,93
Pa-S_054	C-45	CGAGGAGTTTCGGACCCGCTTTGA	6	24	54,2	64,2	82,83
Pa-S_055	C-46	AATAGGACGGGCAGAACGGGCATT	6	24	58,3	66,1	94,95
Pa-S_055	C-Inselspez.-4	GCGCCTTCTCCTCTTGCAGATGT	7	24	54,2	64,4	98,99
Pa-S_056	C-Inselspez.-5	CAGTATGGTACGGACACGGAGCGC	7	24	58,3	66,1	110,111
Pa-S_037	C-spezifisch-1	GCATCATTGCGCGTCACACTCGT	8	24	58,3	66,1	122,123
Pa-S_044	pKL-3	TCTGATCTGGGGCTATCACCTGGA	9	24	54,2	64,4	100,101
Pa-S_045	pKL-7	AATTGATGGCTTCCTCAGGGCCAGG	9	24	54,2	64,4	112,113
Pa-S_046	pKL-11	AGTCATGGACTGAATACGGCGGACT	9	25	52,0	64,6	124,125
Pa-S_042	PAGI-1-1	TTCTCGGTGTCGAGGGATTCTCGG	10	24	58,3	66,1	102,103
Pa-S_043	PAGI-1-3	TGGTACCTCCGACGTACTGGCTG	10	24	58,3	66,1	114,115
Pa-S_047	SG17M-1	CCCGTTGCTCATACCGGTTCCTG	11	24	58,3	66,1	104,105
Pa-S_048	SG17M-4	AGGGCATTCCAGGTGGACTCAGG	11	24	54,2	64,4	116,117
Pa-S_053	fla-insel-1	ACCTGGTGCGCTGGAGGCGATCCT	12	24	58,3	66,1	106,107
Pa-S_049	TB-C47-1	AGCGTCCCTGACCATCCTCATCAG	13	24	58,3	66,1	118,119
Pa-S_050	TB-C47-2	CGCCAACAATTCGGCCATTACAGCG	13	24	54,2	64,4	126,127
Pa-S_051	TB-C47-3	TCCACAGGCAGGAGTACAGGGTG	13	24	58,3	66,1	128,129

FIGURE 18C

				13	24	54,2	64,4	
55	Pa-S_052	TB-C47-4	CGCTGCACATACAGGTCCGTTCTC	13	24	54,2	64,4	130,131
56		Biotin + Cy3-marker						1,12,97,121,132
57	Pa-S_081	oriC T-C_wt_1	AGCCCAGCAATTGCCGTGTTTCTCCG	1	25	65,6	56	
58	Pa-S_082	oriC T-C_mut_2	AGCCCAGCAACTGCCGTGTTTCTCC	1	24	65,1	58	
59	Pa-S_083	alkB2 G-A_wt_2	GCTGCTGGCGGCCGGGTGTGC		19	67,4	79	8,9
60	Pa-S_084	alkB2 G-A_mut_2	TGCTGCTGGCCAGCGGGTGTGCT		21	67,3	67	20,21
61	Pa-S_085	oprl T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG		27	64,6	56	
62	Pa-S_086	oprl T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG		25	64,9	60	
63	Pa-S_087	ampC_1 G-A_wt_2 ampC_1 G-	ACGGCCGCCGGGTGACGCC		19	70,2	84	
64	Pa-S_088	A_mut_2	ACGGGCCGCCAGGTGACGCCG		20	69,9	80	
65	Pa-S_089	ampC_3 C-T_wt_1 ampC_3 C-	GCCGACCTACGCGCCGGGC		19	68,4	84	
66	Pa-S_090	T_mut_2	AGCCGACCTATGCGCCGGGCA		21	68,4	71	
67	Pa-S_091	ampC_4 G-A_wt_2 ampC_4 G-	GTTCGAACGGCTCATGGAGCAGCA		24	65	58	
68	Pa-S_092	A_mut_2	GTTCGAACGACTCATGGAGCAGCAAG		26	63,5	54	
69	Pa-S_093	exoS-1_1	CAGCCCAGTCAGGACGCGCA		20	64,9	70	
70	Pa-S_094	exoU_1	AGTGACGTGCGTTTCAGCAGTCCC		24	64,8	58	
71	Pa-S_095	47D7-1_1	GTGTCACGGCGCCCATGTCTAGCAGC		24	65	63	
72	Pa-S_096	C-46_1	CGAAGTCTGAGGTGTGTGGACCCGC		23	64,5	65	
73	Pa-S_097	Fla-Insel-2_orfA	CGCTGGAGGGTATGTTCCGCAAGG		24	64,8	63	
74	Pa-S_098	Fla-Insel-2_orfC	CGTACTCAGCTTCTCCACCCAGCG		24	64,3	63	
75	Pa-S_099	Fla-Insel-2_orfl	CCTGGACCTCTCCAAGGTTCGCCT		24	65	63	
76	Pa-S_100	Fla-Insel-2_orfJ	GCCATTCCGACGACCAAACAAGGC		24	64,2	58	

group "mother"

FIGURE 19A

No.	tube	name	5'-3'-sequence	group	length	GC-content [%]	Tm [°C]	spot-ID's
1	Pa-S_001	oriC T-C_wt	GAAGCCAGCAAT...GCGGTTCC	1	23	52,2-62,4	52,2;62,4	1,2,3
2	Pa-S_026	oriC T-C_mut_1	GAAGCCCAGCAACTGCGGTTTC	1	23	56,5	64,2	14,15
55	Pa-S_061	oriC T-C_wt_1	AGCCCAGCAATTGCGGTGTTTCTCCG	1	25	65,6	56	13,25
56	Pa-S_062	oriC T-C_mut_2	AGCCCAGCAACTGCGGTGTTCTCC	1	24	65,1	58	37,49
3	Pa-S_057	opr_ T-C_wt_1	GGTGCTCCAGGGTGTTTCGCCGG	1	23	69,6	69,6	4,5
4	Pa-S_058	opr_ T-C_mut_1	GGTGCTCCAGGGCGTTTCGCCGG	1	23	73,9	71,3	16,17
5	Pa-S_059	fliC a-T_wt_1	CAAGATCGCGCGCAGCGGTCAAC	1	22	63,6	65,8	6,7
6	Pa-S_060	fliC a-T_mut_1	CAAGATCGCGCGCTGCGGTCAAC	1	22	63,6	65,8	18,19
59	Pa-S_063	alkB2 G-A_wt_2	GCTGCTGGCGGCGGTGTGC	1	19	67,4	79	8,9
60	Pa-S_064	alkB2 G-A_mut_2	CCTGCTGGCAGGCGGTGTGCT	1	21	67,3	67	20,21
9	Pa-S_063	alkB2 A-G_wt_1	CCTGCCCTGTTCCCACCGCTCTGG	1	25	72,0	72,8	10,11
10	Pa-S_064	alkB2 A-G_mut_1	CTCGCCCTGTTCCGCGCGCCTCTGG	1	24	75,0	73,0	22,23
11	Pa-S_065	citS A-G_wt_1	ACGAGCACTGGCAGAGAAATCCG	1	24	54,2	64,4	26,27
12	Pa-S_066	citS A-G_mut_1	CGAGCACTCCGGAGAGATCCG	1	23	60,9	66,0	38,39
13	Pa-S_067	citS G-C_wt_1	GCGGGAAAACTTCCTGCACATGATGTT	1	26	46,2	63,2	28,29
14	Pa-S_068	citS G-C_mut_1	GCGGAAAACTTCCTCCACATGATGTT	1	26	46,2	63,2	40,41
15	Pa-S_069	oprl T-C_wt_1	AGCTCAGCAGACTGCTGACGAGG	1	23	60,9	66,0	30,31
16	Pa-S_070	oprl T-C_mut_1	AGCTCAGCAGACCGCTGACGAG	1	22	63,6	65,8	42,43
17	Pa-S_085	oprl T-C_wt_2	CAGAAAGCTCAGCAGACTGCTGACGAG	1	27	64,6	56	61,73
18	Pa-S_086	oprl T-C_mut_2	GAAAGCTCAGCAGACCGCTGACGAG	1	25	64,9	60	24,85
19	Pa-S_087	ampC_1 G-A_wt_2	ACGGCCGCGCAGGTGACGCCG	1	25	64,9	60	24,85
	Pa-S_088	ampC_1 G-A_mut_2 / A_mut_2	ACGGCCGCGCAGGTGACGGCC	1	19	70,2	84	32,33
19	Pa-S_019	ampC_2 C-T_wt	GACAAGATGCGGCCTCGACGACC	1	20	69,9	80	44,45
		ampC_2 C-T_mut_1		1	22	63,6	65,8	34,35
20	Pa-S_073	ampC_3 C-T_wt	GACAAGATGCGGTCTCGACGACCG	1	23	60,9	66,0	46,47
21	Pa-S_021	ampC_3 C-T_mut_1	AGCCCGACCTACGCGCGGGCAG	1	22	77,3	71,4	50,51
22	Pa-S_074	T_mut_1	CAGCCGGACCTATGCGCGGGCAG	1	23	73,9	71,3	62,63

FIGURE 19B

No.	Pa-S ID	Name	Sequence			Tm₁	Tm₂	Position
65	Pa-S_089	ampC_3 C-T_wt_1	GCGGACCTACGGCGCGGGC	1	19	68,4	84	36,48
66	Pa-S_090	ampC_3 C-T_mut_2	AGCGGACCTATGGCGCGGGCA	1	21	68,4	71	60,72
67	Pa-S_091	ampC_4 G-A_wt_2	GTTCGAACGGCTCATGGAGCAGCA	1	24	65	58	52,53
68	Pa-S_092	ampC_4 G-A_mut_2	GTTCGAACGACTCATGGAGCAAG	1	26	63,5	54	64,65
25	Pa-S_077	ampC_5 G-C_wt_1	TCGAGCAGCAAGTGTTCCCGGC	1	22	63,6	65,8	54,55
26	Pa-S_078	ampC_5 G-C_mut_1	TGGAGCAGCAACTGTTCCCGGC	1	22	63,6	65,8	66,67
27	Pa-S_027	ampC_6 T-C_wt	GAACAAGACCGGTTCCACCAACGG	1	24	58,3	66,1	56,57
28	Pa-S_079	ampC_7 C-A_wt	AACAAGACCGGCTCACCAACGG	1	23	60,9	66,0	68,69
29	Pa-S_029	ampC_7 C-A_mut_1	GCGACCTGGGCCTGGTGATCCT	1	22	68,2	67,7	58,59
30	Pa-S_080	A_mut_1	GCGACCTGGACTCGTTGTATCCT	1	22	63,6	65,8	70,71
31	Pa-S_031	fliC b	GCCGACCACTGACTCCAACTCG	2	24	58,3	66,1	74,75
32	Pa-S_032	fliC a	GTCCTGCACCGGCACCACTTCA	2	23	56,5	64,2	86,87
33	Pa-S_093	exoS-1_1	CAGCCCAGTCAGGACGGCGCAA	3	20	64,9	70	76,77
34	Pa-S_094	exoU	CGGCAGTTTGAGACGGAGTCACC	3	24	58,3	66,1	88,89
70	Pa-S_034	exoU_1	AGTCACGTGCGTTCAGCAGTCCC	3	24	64,8	58	84,96
35	Pa-S_036	C-47-1	GCGGCGATCTTCTCCACCTCATCCGG	4	24	54,2	64,4	78,79
77	Pa-S_095	47D7-1_1	GTGTCACCGGCCCATGTCTAGCAGC	5	24	65	63	80,81
38	Pa-S_041	47D7-2	GTGAGCATGAATCGGACTCGGT	5	24	58,3	66,1	92,93
39	Pa-S_054	C-45	CCGAGCAGTTCGGACCGGCTTTGCA	6	24	54,2	64,4	82,83
40	Pa-S_055	C-45	AATAGGACGGGCAGAACGGGGCATT	6	24	58,3	66,1	94,95
41	Pa-S_056	C-45_1	CGAAGCTGAGGTGTGGACCCGC	6	23	64,5	65	108,120
42	Pa-S_035	C-Inselspez-4	GCGGCTTCTCCTCTTTGCAGATGT	7	24	54,2	64,4	98,99
43	Pa-S_037	C-spezifisch-1	CAGCATGGTACGGACACGAAGCGC	7	24	58,3	66,1	110,111
44	Pa-S_044	pKL-3	GCATCATTGGCGCGTCAGATCTGGT	8	24	58,3	66,1	122,123
45	Pa-S_046	pKL-11	TCTGAACGGCGGGCTATCACCTGGA	9	24	54,2	64,4	100,101
47	Pa-S_042	PAGI-1-1	AGTCACGGGACTGGAATACGGCGACT	9	25	52,0	64,6	124,125
48	Pa-S_043	PAGI-1-8	TTCTCGGTGTCGAGGGATTCTCGG	10	24	58,3	66,1	102,103
			TGGTAGCTCTCGCGCTACTGGGCTG	10	24	58,3	66,1	114,115

FIGURE 19C

FIGURE 20

Chip: MHH_P_aer_array2 (12x11 array with spot distance of 19.00 mm)

56	43	43	46	46	76	76	54	54	55	55	56
	42	42	74	74	48	48	50	50	75	75	72
56	41	41	44	44	47	47	49	49	51	51	72
62	32	32	34	34	73	73	38	38	40	40	70
61	31	31	69	69	35	35	71	71	39	39	70
61	22	22	68	68	26	26	28	28	30	30	66
58	21	21	67	67	25	25	27	27	29	29	66
58	12	12	14	14	16	16	64	64	20	20	65
57	11	11	13	13	15	15	63	63	19	19	65
57	2	2	4	4	6	6	60	60	10	10	62
56	1	1	3	3	5	5	59	59	9	9	56

FIGURE 21

Chip occupancy

marker spot	C-spezifisch-1	pKL-11	Fla-Insel-2 orfJ	TB-C47-3	TB-C47-4	marker spot
	C-Inselspezifisch-5	Fla-Insel-2 orfC	PAGI-1-8	SG17M-4	Fla-Insel-2 orfl	C-46_1
marker spot	C-Inselspezifisch-4	pKL-3	PAGI-1-1	SG17M-1	fla-Insel-1	C-46_1
	flic A	exoU	Fla-Insel-2 orfA	47D7-2	C-46	exoU_1
	flic B	exoS-1_1	C-47-1	47D7-1_1	C-45	exoU_1
mut_2 oprl T-C wt_2 oprl T-C wt_2	mut_1 ampC_3 C-T wt	mut_2 ampC_4 G-A wt_2	mut_1 ampC_5 G-C wt_1	mut_1 ampC_6 T-C wt	mut_1 ampC_7 C-A wt	mut_2 ampC_3 C-T
mut_2 oriC T-C wt_2 oriC T-C wt_1 oriC T-C	mut_1 citS A-G wt_1	mut_1 citS G-C wt_1	mut_1 oprl T-C wt_1	mut_2 ampC_1 G-A wt_2	mut_1 ampC_2 C-T wt	mut_2 ampC_3 C-T wt_1 ampC_3 C-T wt_1
wt_1	mut_1 oriC T-C wt	mut_1 oprL T-C wt_1	mut_1 fliC a A-T wt_1	mut_2 alkB2 G-A wt_2	mut_1 alkB2 A-G wt_1	oprl T-C mut_2
marker spot						marker spot